

LX

9	18	27	36	45	54
CTC GAG ATG CAG AGG AAC CTG GGA GCT GTG CTG GGG ATT CTG TGG GTG CAG ATT					
L E M Q R N L G A V L G I L W V Q I					
63	72	81	90	99	108
TGC TGG CTG AAA GAA CAG CAA GTG CAG CAG AGT CCC GCA TCC TTG GTT CTG CAG					
C W L K E Q Q V Q Q S P A S L V L Q					
117	126	135	144	153	162
GAG GGG GAG AAC GCA GAG CTC CAG TGT AGC TTT TCC ATC TTT ACA AAC CAG GTG					
E G E N A E L Q C S F S I F T N Q V					
171	180	189	198	207	216
CAG TGG TTT TAC CAA CGT CCT GGG GGA AGA CTC GTC AGC CTG TTG TAC AAT CCT					
Q W F Y Q R P G G R L V S L L Y N P					
225	234	243	252	261	270
TCT GGG ACA AAG CAG AGT GGG AGA CTG ACA TCC ACA ACA GTC ATT AAA GAA CGT					
S G T K Q S G R L T S T T V I K E R					
279	288	297	306	315	324
CGC AGC TCT TTG CAC ATT TCC TCC CAG ATC ACA GAC TCA GGC ACT TAT CTC					
R S S L H I S S S Q I T D S G T Y L					
333	342	351	360	369	378
TGT GCC TCA AAT TCT GGA GGA AGC AAT GCA AAG CTA ACC TTC GGG AAA GGC ACT					
C A S N S G G S N A K L T F G K G T					
387	396	405	414	423	432
AAA CTC TCT GTT AAA TCA GGT GGC GGA GGG TCT GGC GGG GGT GGA TCC GGG GGT					
K L S V K S G G G S G G G G S G G					
LINKER					
441	450	459	468	477	486
GGA GGC TCA GAG GCT GCA GTC ACC CAA AGC CCA AGA AAC AAG GTG GCA GTA ACA					
G G S E A A V T Q S P R N K V A V T					
495	504	513	522	531	540
GGA GGA AAG GTG ACA TTG AGC TGT AAT CAG ACT AAT AAC CAC AAC AAC ATG TAC					
G G K V T L S C N Q T N N H N N M Y					
549	558	567	576	585	594
TGG TAT CGG CAG GAC ACG GGG CAT GGG CTG AGG CTG ATC CAT TAT TCA TAT GGT					
W Y R Q D T G H G L R L I H Y S Y G					
603	612	621	630	639	648
GCT GGC AGC ACT GAG AAA GGA GAT ATC CCT GAT GGA TAC AAG GCC TCC AGA CCA					
A G S T E K G D I P D G Y K A S R P					

VK

VK

AGC CAA GAG AAC TTC TCC CTC ATT TTG GAG TTG CCT ACC CCC TCT CAT ACA TCA FIGURE

S Q E N F S L I L E L A T P S Q T S

711 720 729 738 747 756

GTG TAC TTC TGT GCC AGC GGT GAG ACA GGG ACC AAC GAA AGA TTA TTT TTC GGT

V Y F C A S G E T G T N E R L F F G

765 774 783 ~~784~~ 792 801 810

CAT GGA ACC AAG CTG TCT GTC CTG ~~ACT~~ AGT AAC TCC ATC ATG TAC TTC AGC CAC

H G T K L S V L T S N S I M Y F S H

819 828 837 846 855 864

TTC GTG CCG GTC TTC CTG CCA GCG AAG CCC ACC ACG ACG CCA GCG CCG CGA CCA

F V P V F L P A K P T T T P A P R P

873 882 891 900 909 918

CCA ACA CCG GCG CCC ACC ATC GCG TCG CAG CCC CTG TCC CTG CGC CCA TCT AGT

P T P A P T I A S Q P L S L R P S S

~~Abcgt~~ 927 936 945 954 963 972

TCT AGA GAT CCC AAA CTC TGC TAC CTG CTG GAT GGA ATC CTC TTC ATC TAT GGT

S R D P K L C Y L L D G I L F I Y G

981 990 999 1008 1017 1026

GTC ATT CTC ACT GCC TTG TTC CTG AGA GTG AAG TTC AGC AGG AGC GCA GAC GCC

V I L T A L F L R V K F S R S A D A

1035 1044 1053 1062 1071 1080

CCC GCG TAC CAG CAG GGC CAG AAC CAG CTC TAT AAC GAG CTC AAT CTA GGA CGA

P A Y Q Q G Q N Q L Y N E L N L G R

1089 1098 1107 1116 1125 1134

AGA GAG GAG TAC GAT GTT TTG GAC AAG AGA CGT GGC CGG GAC CCT GAG ATG GGG

R E E Y D V L D K R R G R D P E M G

1143 1152 1161 1170 1179 1188

GGA AAG CCG AGA AGG AAG AAC CCT CAG GAA GGC CTG TAC AAT GAA CTG CAG AAA

G K P R R K N P Q E G L Y N E L Q K

1197 1206 1215 1224 1233 1242

GAT AAG ATG GCG GAG GCC TAC AGT GAG ATT GGG ATG AAA GGC GAG CGC CGG AGG

D K M A E A Y S E I G M K G E R R R

1251 1260 1269 1278 1287 1296

GGC AAG GGG CAC GAT GGC CTT TAC CAG GGT CTC AGT ACA GCC ACC AAG GAC ACC

G K G H D G L Y Q G L S T A T K D T

1305 1314 1323 1332 ~~1341~~ 1350

TAC GAC GCC CTT CAC ATG CAG GCC CTG CCC CCT CGC TAA ~~GCG~~ ~~GCC~~ ACC GCG

Y D A L H M Q A L P P R * A A A T A

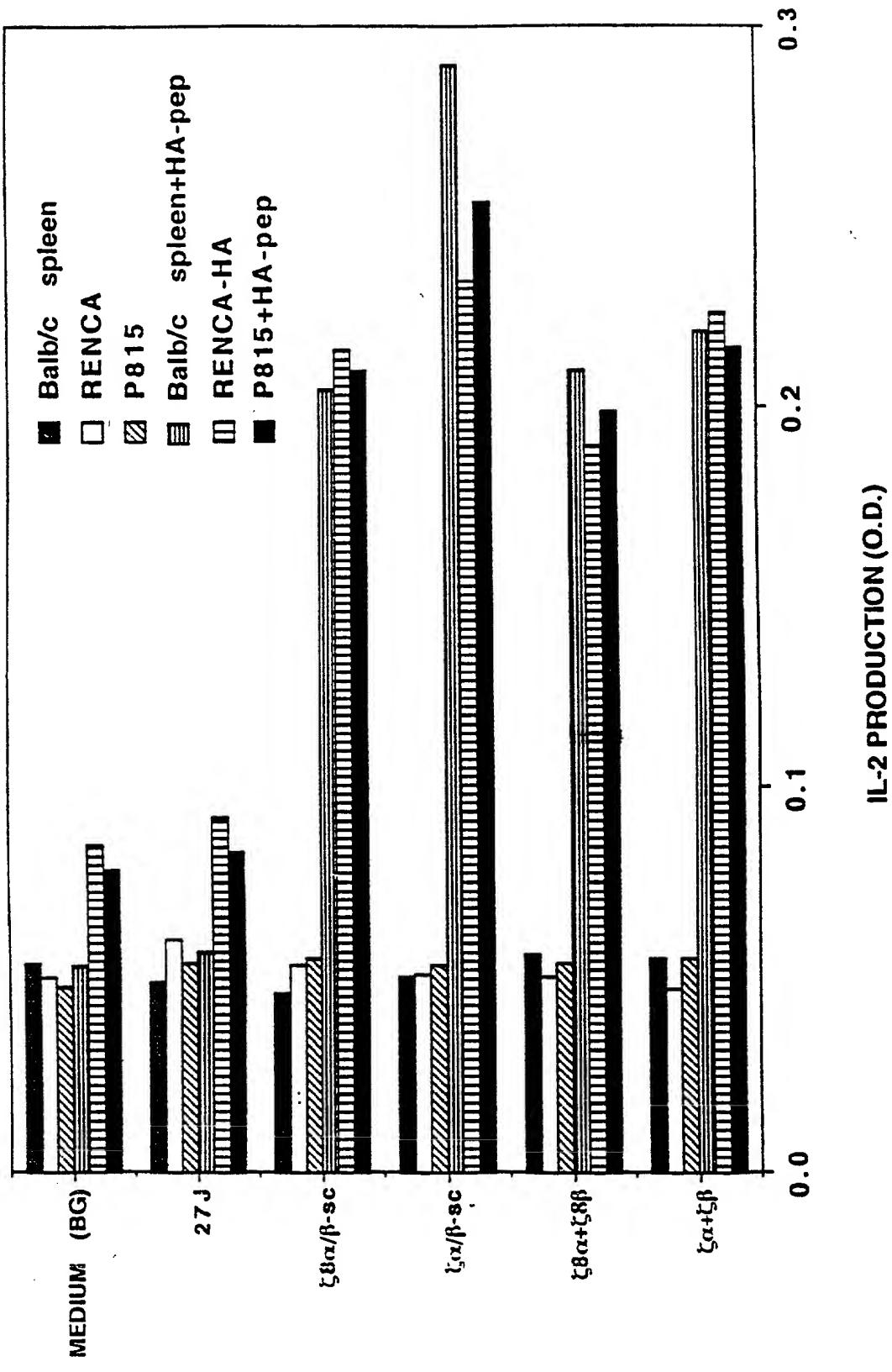
STOP

3B

CD8

CD8 HINGE

2 chain



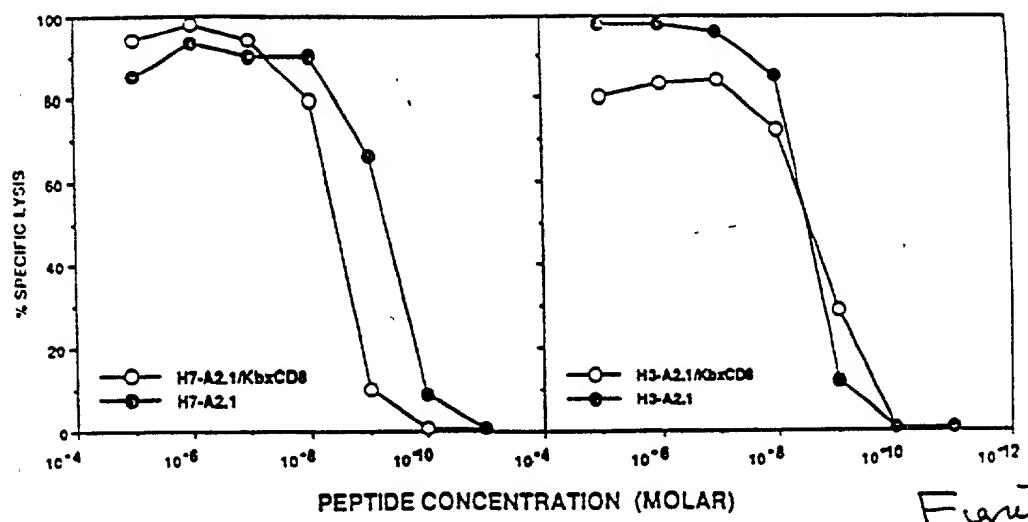


Figure 5

Va1 CCC AAG GCA CTG ATG TTC ATC TTC
 Va2 TGA GAC AAA GTC CCC AAT CTC TGA CAG
 Va3 CTG CAG CTG CTC CTC AAG TAC TAT TC
 Va4.1,2,3 TCC CGG AGA AGG TCC ACA GTT CCT CTT T
 Va4.4 GAA GCA GCA GAG GGT TTG AAG CCA CAT AC

2.
 Va5 GGC AGG TCT TCA GTT GCT TAT GAA GGT
 Va6 GGT TCC TCT TCA GGG TCC AGA ATA TCT
 Va7 GCG AAG AAC TCA CCC TGG ACT GTT CAT
 Va8 GAG CTC CAC AGA CAA CAA GAC GAC CGA GCA
 Va9 GAG CTG CGA CGT TCC TTA GTG ACT GTG

3.
 Va10 CCT CGT CAG CCT GTT GTC CAA TCC TTC TGG
 Va11 CAG CCT CAT CAA TCT GTT CTA CTT GGC T
 Va12 CCA CCA GGG ACC ACA GTT TAT CAT TCA A
 Va14 ACC TGG AGA GAA TCC TAA GCT CAT CAT
 Va15 AGG TCT TGT GTC CCT GAC AGT CCT GGT T

4.
 Va16 CAA GCA AAC ACT GTA GTG CAG AGC CCT TCC
 Va17 CAA GAC ATC CAT AAC TGC CCT ACA G
 Va18 GTG TAT GAA ACC CAG GAC AGT TCT TAC
 Va19 CCG TAT TTC TTT CTT ATG TTG TTT TGG AT
 Va20 CAA AGC TCT CCA TCG CTG ACT GTT CAA G

Beta Groups

1.
 V β 1 ATC TAA TCC TGG GAA GAG CAA AT
 V β 2 GGC GTC TGG TAC CAC GTG GTC AA
 V β 3 GTG AAA GGG CAA GGA CAA AAA GC
 V β 4 GAT ATG CGA ACA GTA TCT AGG C
 V β 5.1 ACA TAA TCA AAG GAA AGG GAG AA

2.
 V β 6 TCC TGA TTG GTC AGG AAG GGC AA
 V β 7 TAC CTG ATC AAA AGA ATG GGA GA
 V β 8.1 ATA ACC ATG ACA ATA TGT ACT GG
 V β 8.2 ATA ACC ACA ACA TGT ACT GG
 V β 8.3 ATA GCC ACA ACT ACA TGT ACT GG

3.
 V β 9 AGC TTG CAA GAG TTG GAA AAC CA
 V β 10 GAT TAT GTT TAG CTA CAA TAA TA
 V β 11 ACA AGG TGA CAG GGA AGG GAC AA
 V β 12 ACC TAC AGA ACC CAA GGA CTC AG
 V β 13 CAG TTG CCC TCG GAT CGA TTT TC

4.
 V β 14 GCC GAG ATC AAG GCT GTG GGC AG
 V β 15 AGA ACC ATC TGT AAG AGT GGA AC
 V β 16 CAT CAA ATA ATA GAT ATG GGG CA
 V β 17 GTA GTC CTG AAA AAG GGC ACA CT
 V β 18 CAT CTG TCA AAG TGG CAC TTC A

Range : 1 - 393 Mo : Normal
odon Table : Universal

FIG. 7A

File Name : h7-beta
Page : 1 - 402 Mr. : Normal
odon Table : Universal

FIG 7B

9 18 27 36 45 54
ATG GGC TCC AGA CTC TTC TTT GTG GTT TTG ATT CTC CTG TGT GCA AAA CAC ATG
Met Gly Ser Arg Leu Phe Phe Val Val Leu Ile Leu Leu Cys Ala Lys His Met

63 72 81 90 99 108
GAG GCT GCA GTC ACC CAA AGT CCA AGA AGC AAG GTG GCA GTA ACA GGA GGA AAG
Glu Ala Ala Val Thr Gln Ser Pro Arg Ser Lys Val Ala Val Thr Gly Gly Lys

117 126 135 144 153 162
GTG ACA TTG AGC TGT CAC CAG ACT AAT AAC CAT GAC TAT ATG TAC TGG TAT CGG
Val Thr Leu Ser Cys His Gln Thr Asn Asn His Asp Tyr Met Tyr Trp Tyr Arg

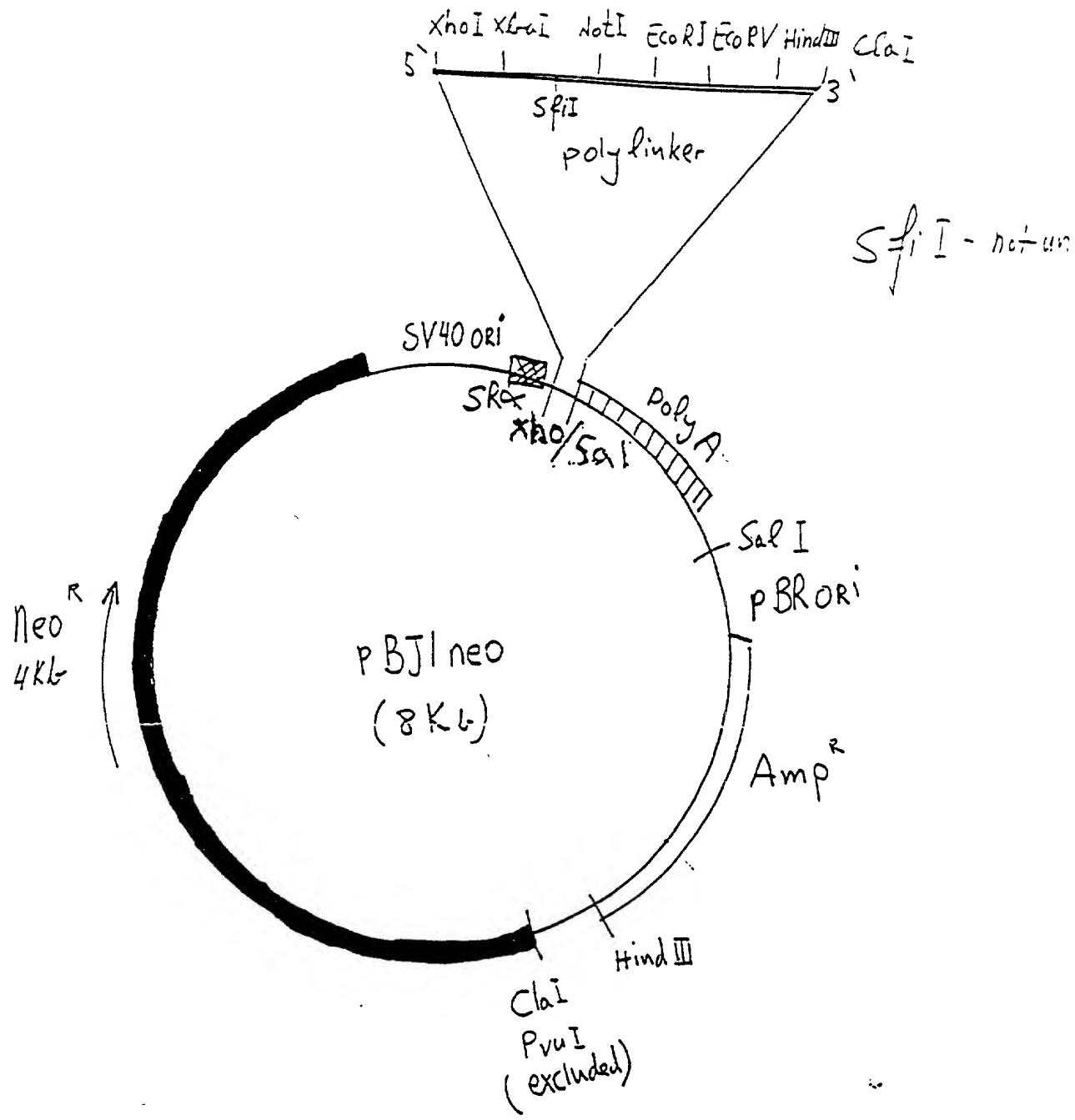
171 180 189 198 207 216
CAG GAC ACG GGG CAT GGG CTG AGG CTG ATC CAT TAC TCA TAT GTC GCT GAC AGC
Gln Asp Thr Gly His Gly Leu Arg Leu Ile His Tyr Ser Tyr Val Ala Asp Ser

225 234 243 252 261 270
ACG GAG AAA GGA GAT ATC CCT GAT GGG TAC AAG GCC TCC AGA CCA AGC CAA GAG
Thr Glu Lys Gly Asp Ile Pro Asp Gly Tyr Lys Ala Ser Arg Pro Ser Gln Glu

279 288 297 306 315 324
AAT TTC TCT CTC ATT CTG GAG TTG GCT TCC CTT TCT CAG TCA GCT GTA TAT TTC
Asn Phe Ser Leu Ile Leu Glu Leu Ala Ser Leu Ser Gln Ser Ala Val Tyr Phe

333 342 351 360 369 378
TGT GCC AGC AGC GAT TTC GCC GGG ACA GGG GGC TTC TAT GAA CAG TAC TTC GGT
Cys Ala Ser Ser Asp Phe Ala Gly Thr Gly Gly Phe Tyr Glu Gln Tyr Phe Gly

387 396
CCC GGC ACC AGG CTC ACG GTT TCT 3'
Pro Gly Thr Arg Leu Thr Val Ser



pBJ1neo - MCB 8: 466, 1988

Polylinker - Science, 249: 677, 1990

